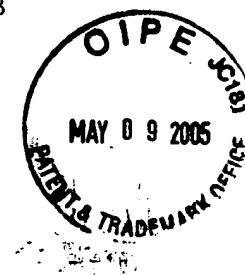Alignment: Global Protein alignment against reference molecule
Parameters: Scoring matrix: BLOSUM 62

    Reference molecule: SEQIDNO:6, Region 1-451
    Number of sequences to align: 2
    Settings: Similarity significance value cutoff: >= 60%

Summary of Percent Matches:
    Reference: SEQIDNO:6   1 -   451   (451 aa)   --
    Sequence 2:   Kimura Tri101 Pro   1 -   451   (451 aa)   99%

```
SEQIDNO:6        1  mafkiqldtlgqlpgllsiytqislllypvsdssqyptivstfeqglkrfseavpwvagqv
Kimura Tri10     1  mafkiqldtlgqlpgllsiytqislllypvsdpsqyptivstfeqglkrfseavpwvagqv

SEQIDNO:6       61  kaegisegntgtsfivpfedvprvvvkdlrddpsaptiegmrkagypmamfdeniiaprk
Kimura Tri10    61  kaegisegntgtsfivpfedvprvvvkdlrddpsaptiegmrkagypmamfdeniiaprk

SEQIDNO:6      121  tlpigpgtgpddpkpvillqlnfikgglilltvngqhgamdmvgqdavirlllskacrndpf
Kimura Tri10   121  tlpigpgtgpddpkpvillqlnfikgglilltvngqhgamdmvgqdavirlllskacrndpf

SEQIDNO:6      181  teeemtamnldrktivpylenytigpevdhqivkadvaggdavltpvsaswafftfspka
Kimura Tri10   181  teeemtamnldrktivpylenytigpevdhqivkpdvaggdavltpvsaswaffkfspka

SEQIDNO:6      241  mselkdaatktldastkfvstddalsafiwksasrvrleridgsaptefcravdarpamg
Kimura Tri10   241  mselkdaatktldastkfvstddalsafiwksasrvrleridgsaptefcravdarpamg

SEQIDNO:6      301  vsnnypgllqnmtyhnstigeianeslgatasrlrseldpasmrqrtrglatylhnnpdk
Kimura Tri10   301  vsnnypgllqnmtyhnstigeianeslgatasrlrseldpasmrqrtrglatylhnnpdk

SEQIDNO:6      361  snvsltadadpstsvmlsswakvglwdydfglglgkpetvrrpifepveslmyfmpkkpd
Kimura Tri10   361  snvsltadadpstsvmlsswakvglwdydfgfglgkpetvrrpifepveslmyfmpkkpd

SEQIDNO:6      421  gefcaalslrdedmdrlkadkewtkyaqyvg
Kimura Tri10   421  gefcaalslrdedmdrlkadkewtkyaqyvg
```